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The alignment was done on 3 Protein sequences.

Character to show that a position in the alignment is perfectly conserved: '*'

Character to show that a position is well conserved: '.'

Alignment

ADIPROT	MSVFDSKFKGIHVYSEIGELESVLVHEPGREIDYITPARLDELLFSAILE	50
ARTADIPRO	MSVFDSKFKGIHVYSEIGELESVLVHEPGREIDYITPARLDELLFSAILE	50
HOMADIPRO	MSVFDSKFKGIHVYSEIGELETVLVHEPGREIDYITPARLDELLFSAILE	50

ADIPROT	SHDARKEHKQFVAELKANDINVVELIDLVAETYDLASQEAQDKLIEEFLE	100
ARTADIPRO	SHDARKEQSQFVAILKANDINVVETIDLVAETYDLASQEAQDKRLIEEFLE	100
HOMADIPRO	SHDARKEHQSFVKIMKDRGINVVELTDLVAETYDLASKAAKEEFIFTFLE	100

ADIPROT	DSEPVLSSEHKVVRNFKAKKTSRKLVEIMMAGITKYDLGIEADHELIV	150
ARTADIPRO	DSEPVLSSEAHKKVVRNFKAKKTSRKLVELMMAGITKYDLGVEADHELIV	150
HOMADIPRO	ETVPVLTEANKKAVRAFLLSKPT-HEMVEFMMSGITKYELGVESENELIV	149
	..***	
ADIPROT	DPMPNLYFTRDPFASVGNVGTIHYMRYKVRQRETLSRFVFSNHPKLINT	200
ARTADIPRO	DPMPNLYFTRDPFASVGNVGTIHFMYKVRRETLSRFVFRNHPKLVNT	200
HOMADIPRO	DPMPNLYFTRDPFASVGNVGTIHFMYIVRRRETLEFARFVFRNHPKLVKT	199

ADIPROT	PWYYDPSLKLSIEGGDVFIYNNDTLVVGVSERTDLQTVTLAKNIVANKE	250
ARTADIPRO	PWYYDPAMKLSIEGGDVFIYNNDTLVVGVSERTDLDTVTLLAKNLVANKE	250
HOMADIPRO	PWYYDPAMKMPIEGGDVFIYNNETLVVGVSERTDLDTITLLAKNIKANKE	249

ADIPROT	CEFKRIVAINVPKWTNLMHLDTWLTMLDKDKFLYSPIANDVFKFWDYDLV	300
ARTADIPRO	CEFKRIVAINVPKWTNLMHLDTWLTMLDKNKFLYSPIANDVFKFWDYDLV	300
HOMADIPRO	VEFKRIVAINVPKWTNLMHLDTWLTMLDKNKFLYSPIANDVFKFWDYDLV	299

ADIPROT	NGGAEPQPVENGLPLEGLLQSIINKKPVLIPIAGEGASQMEIERETHFDG	350
ARTADIPRO	NGGAEPQPVENGLPLEKLLQSIINKKPVLIPIAGEGASQMEIERETHFDG	350
HOMADIPRO	NGGAEPQPOLNGLPLDKLLASIINKEPVLIPIGGAGATEMEIARETNFDG	349

ADIPROT	TNYLAIRPGVVIGYSRNEKTNAALEAAGIKVLPFHGNQLSLGMGNARCMS	400
ARTADIPRO	TNYIAIRPGVVIGYSRNEKTNAALKAAGIKVLPFHGNQLSLGMGNARCMS	400
HOMADIPRO	TNYLAIKPGLVIGYDRNEKTNAALKAAGITVLPFHGNQLSLGMGNARCMS	399

ADIPROT	MPLSRKDVKW 410	
ARTADIPRO	MPLSRKDVKW 410	
HOMADIPRO	MPLSRKDVKW 409	

FIG. 1

ADIPROT	=	Mycoplasma arginini
ARTADIPRO	=	Mycoplasma arthritides
HOMADIPRO	=	Mycoplasma hominus

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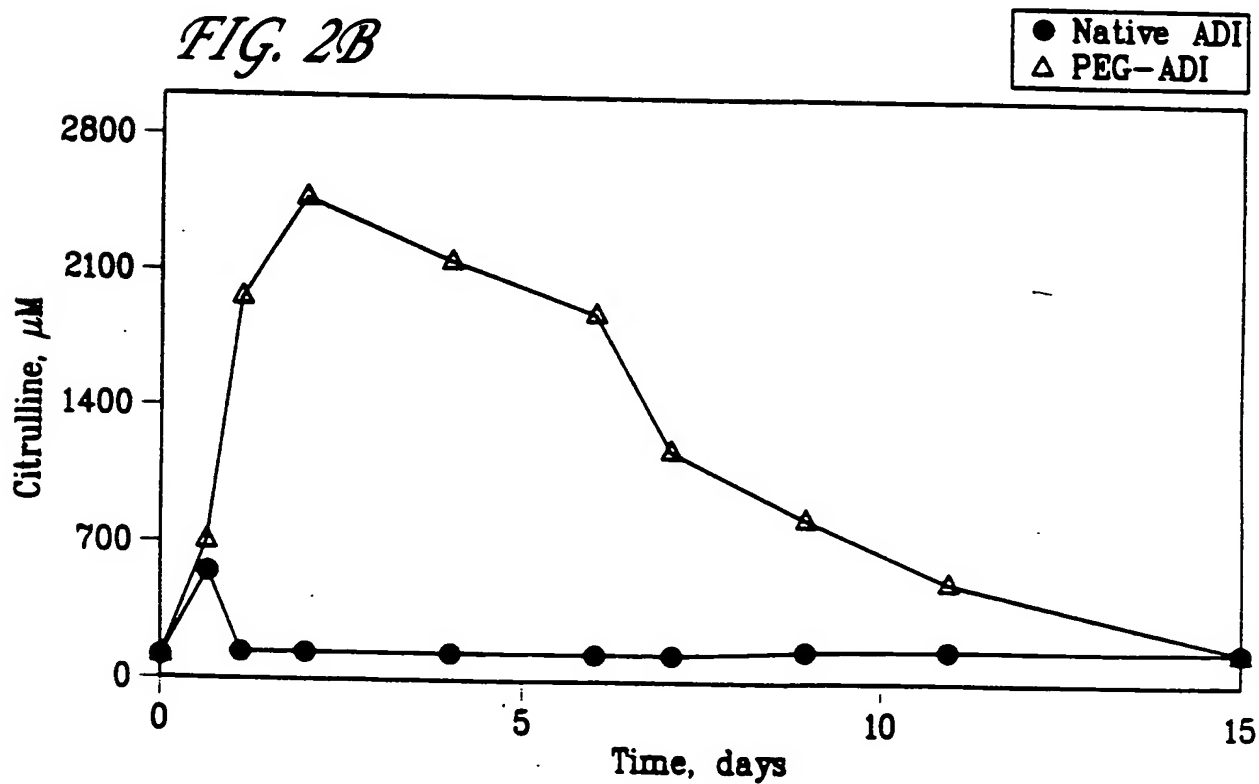
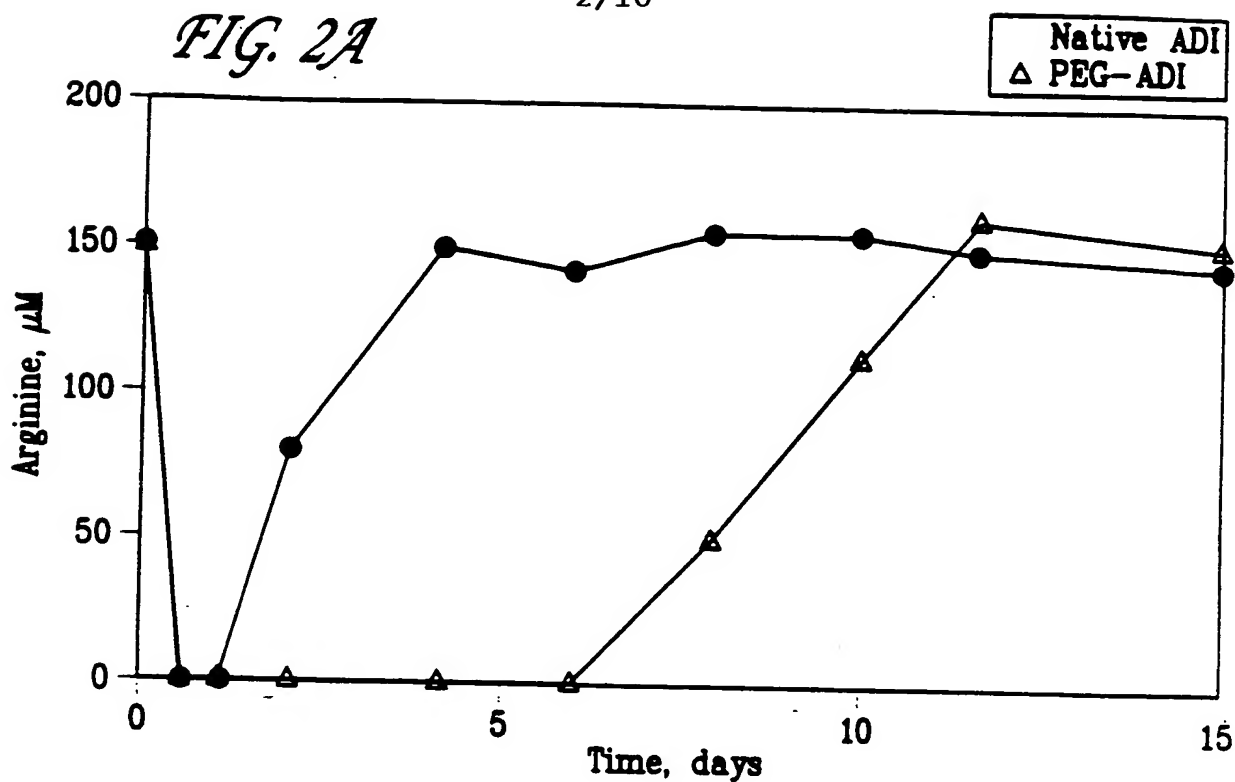


FIG. 3 3/10

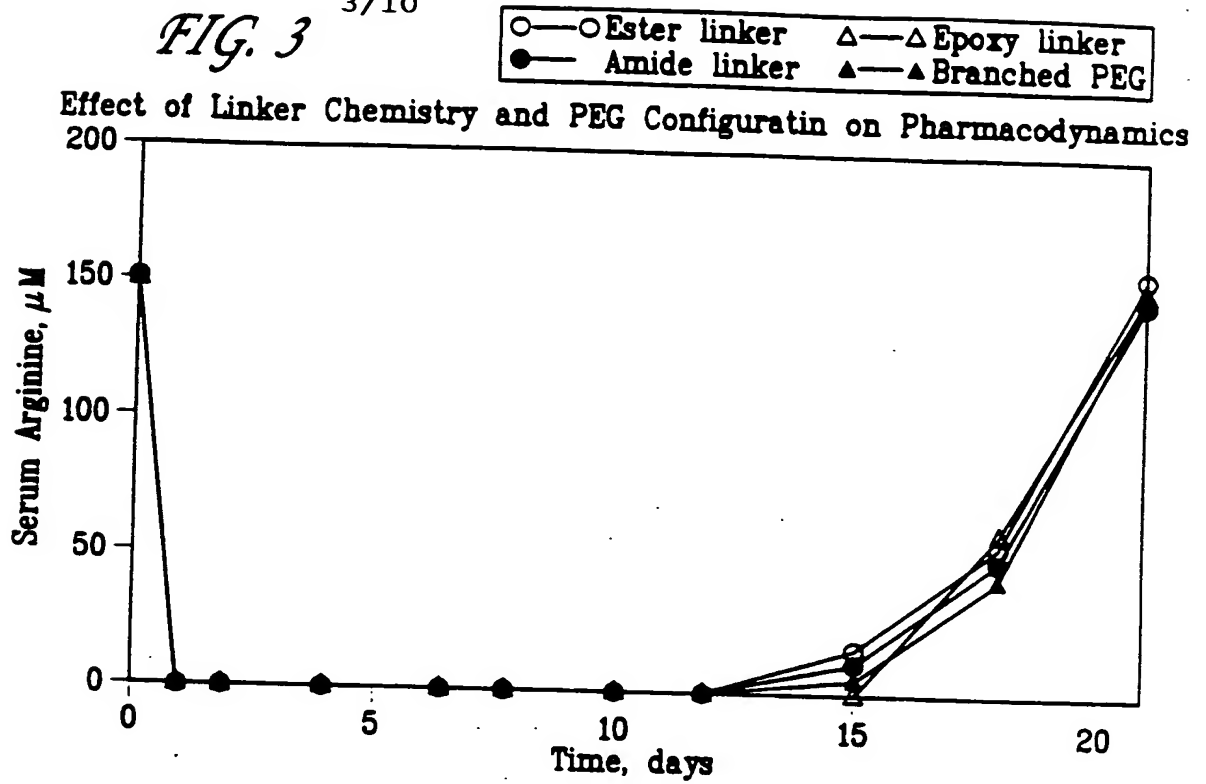
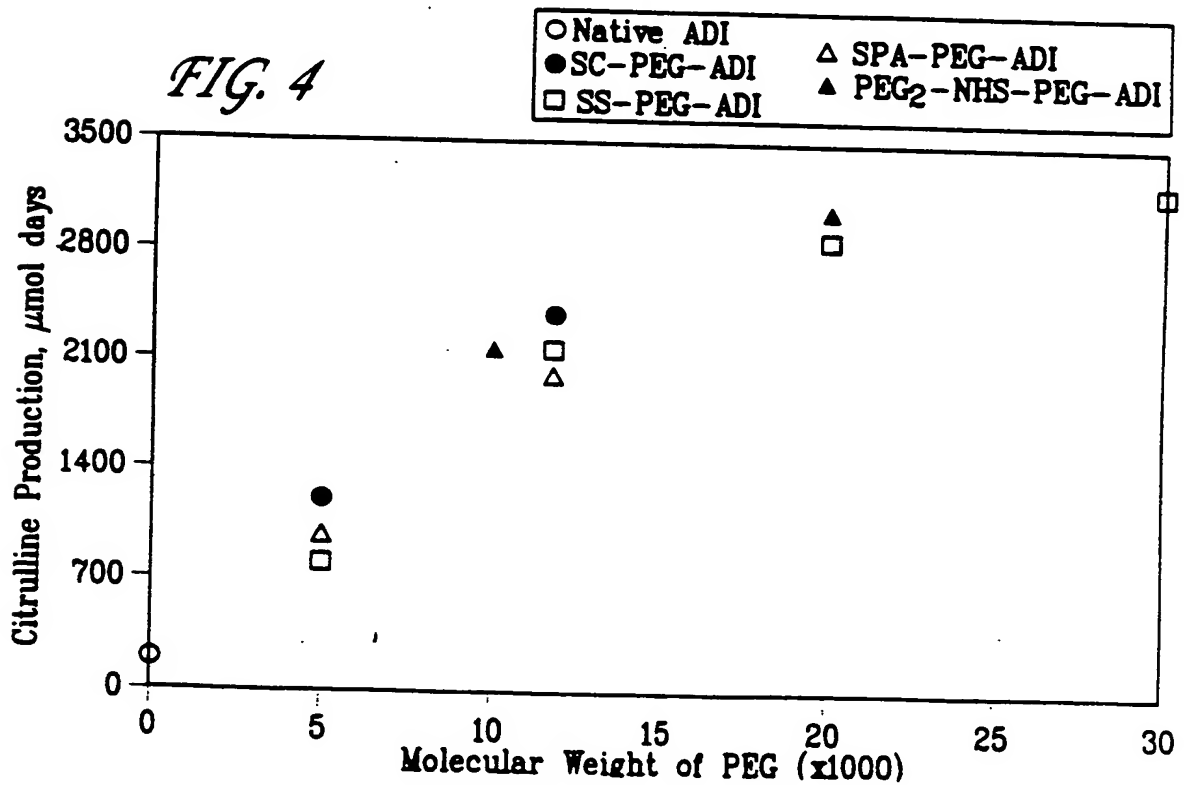
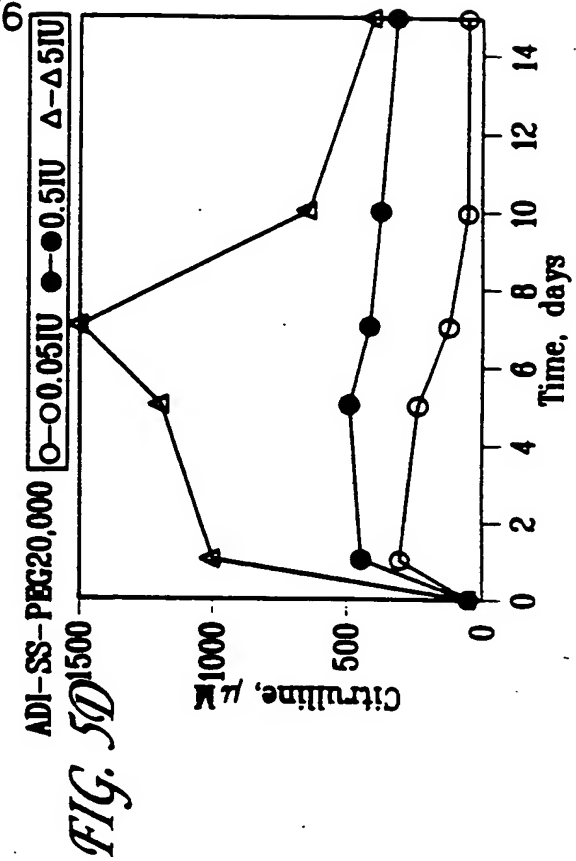
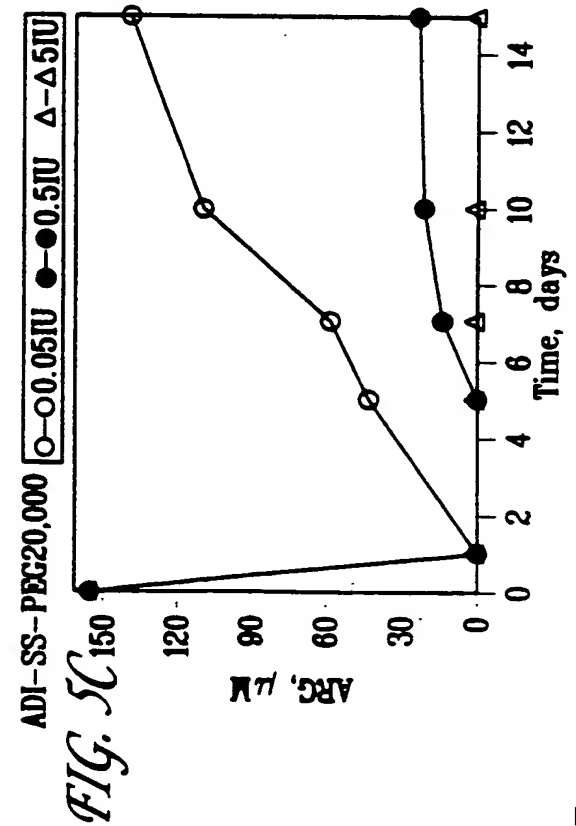
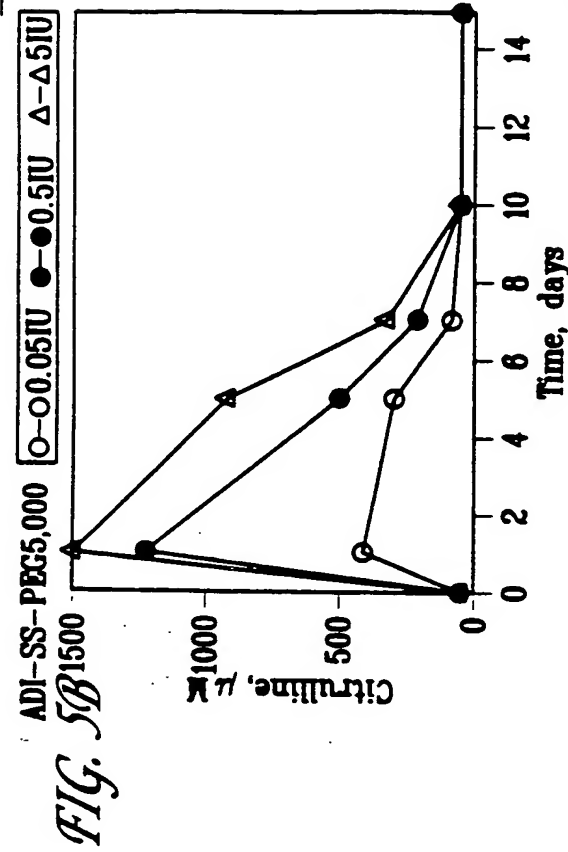
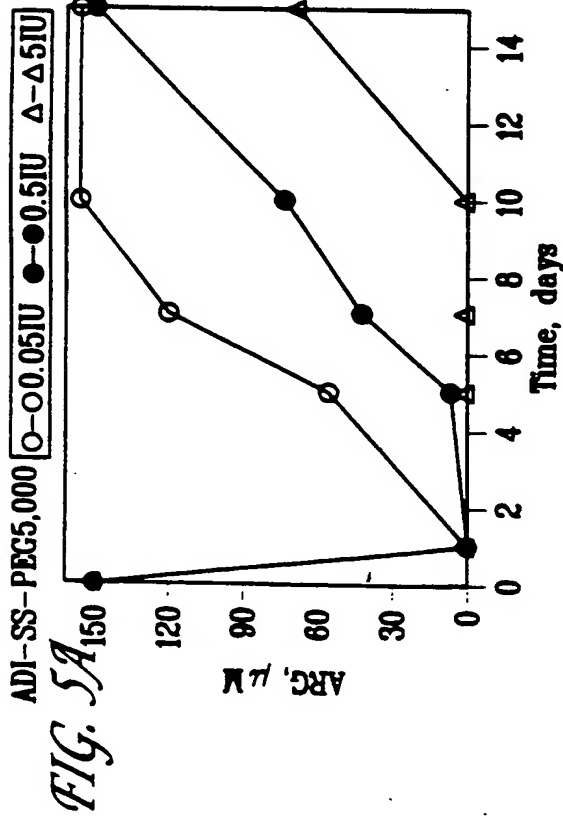


FIG. 4





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FIG. 6

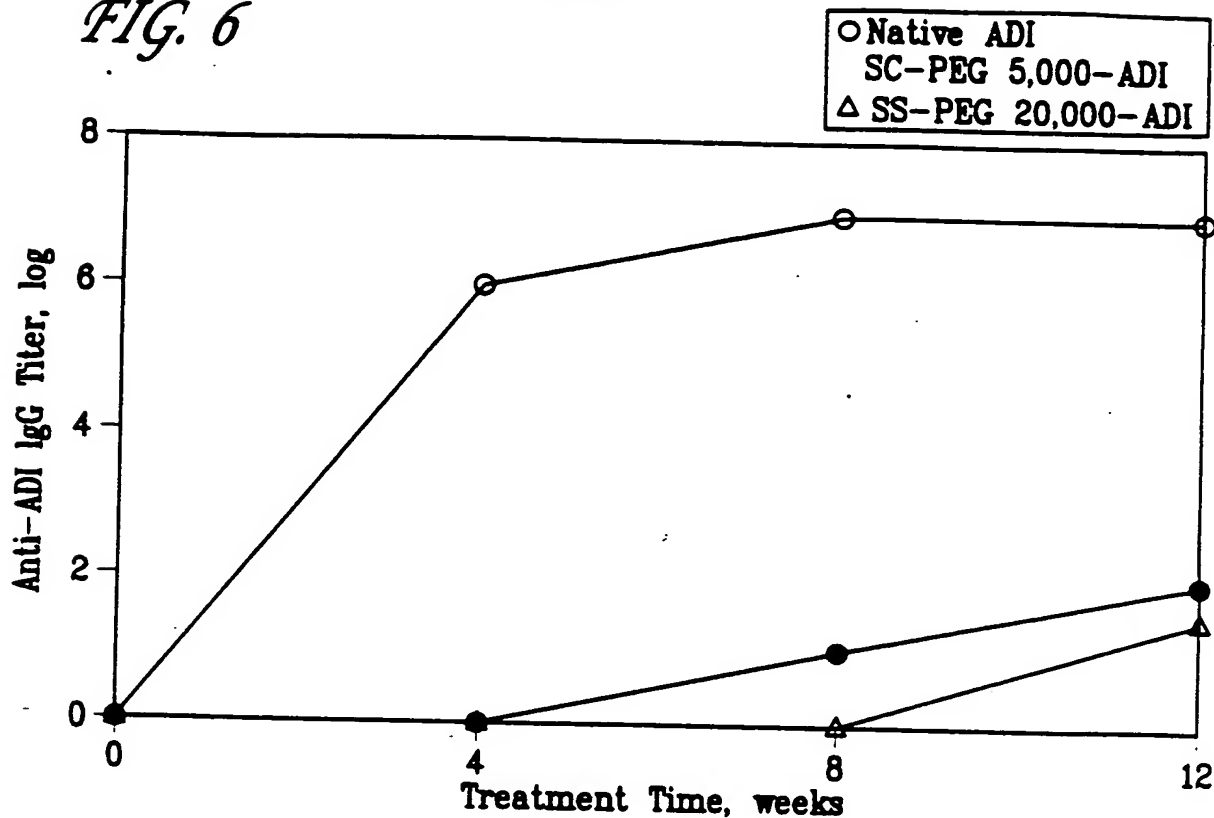
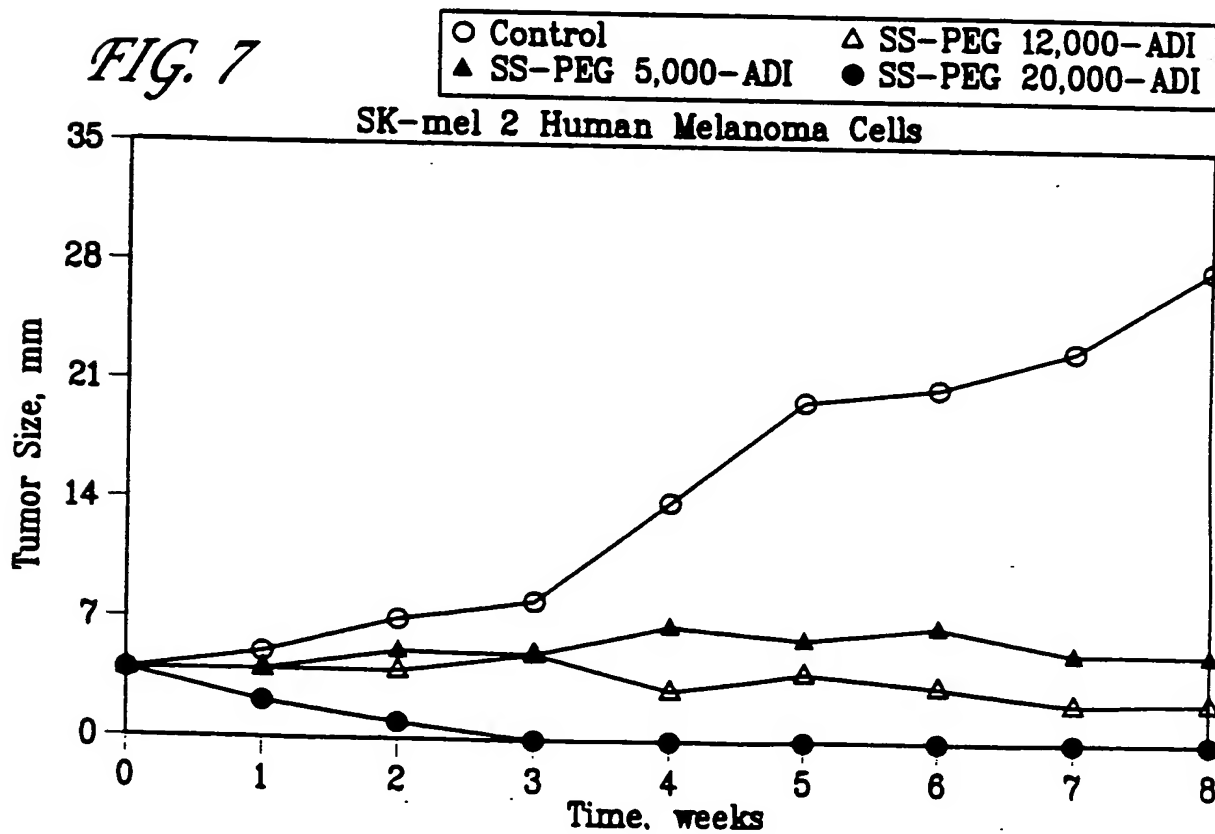


FIG. 7



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FIG. 8

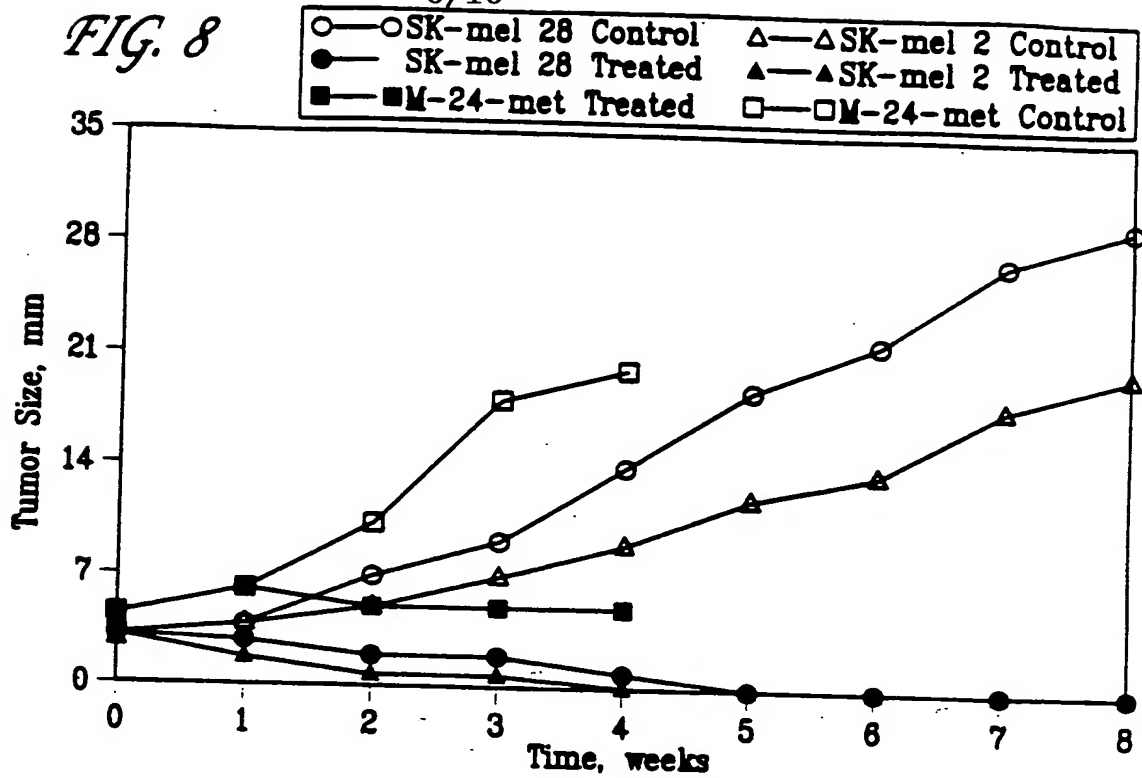
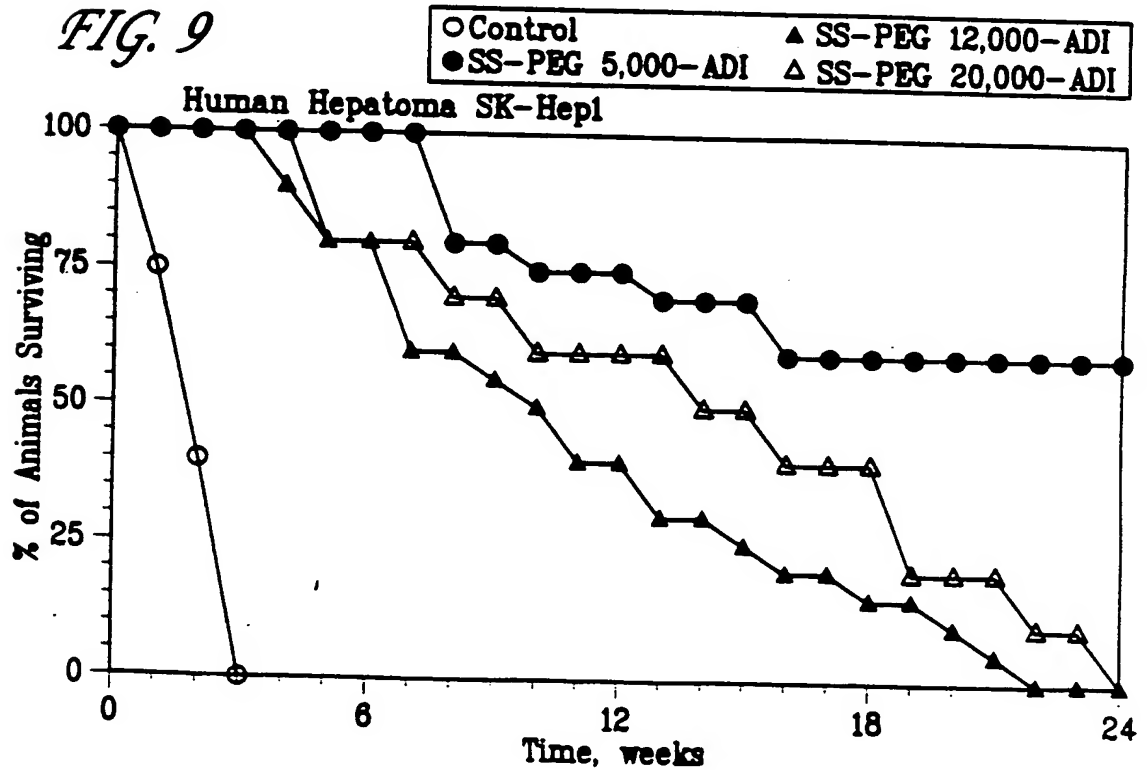


FIG. 9



The alignment was done on 2 amino acid sequences. 7/10

Alignment

STRADIPYR	MTAQTPIHVYSEIGKLKKVLLHRPGKEIENLMPDYLERLLFDDIPFLEDA	50
STRADIPNE	MSSHPIQVFSEIGKLKKVMLHRPGKELENLLPDYLERLLFDDIPFLEDAQ	50
STRADIPYR	QKEHDAFAQALRDEGIEVLYLETLAAESLVTPEIREAFIDEYLSEANIRG	100
STRADIPNE	KEHDAFAQALRDEGIEVLYLEQLAAESLTSPEIRDQFIEEYLDEANIRDR	100
STRADIPYR	RATKKAIRELLMAIEDNQELIEKTMAGVQKSELPEIPASEKGLTDLVESN	150
STRADIPNE	QTKVAIRELLHGIKDNQELVEKTMAGIQKVELPEIPDEAKDLTDLVESEY	150
STRADIPYR	YPFAIDPMPNLYFTRDPFATIGTGVSLSNHMFSETRNRETLYGKYIFTHHP	200
STRADIPNE	PFAIDPMPNLYFTRDPFATIGNAVSLNHMFADTRNRETLYGKYIFKYHPI	200
STRADIPYR	IYGGGKVPVMVYDRNETTRIEGGDELVLSKDVLA VGISQRTDAASIEKLLV	250
STRADIPNE	YGGKVDLVYNREEDTRIEGGDELVLSKDVLA VGISQRTDAASIEKLLVNI	250
STRADIPYR	NIFKQNLGFKKVLAFEFANNRKFMHLDTVFTMVDYDKFTIHPEIEGDLRV	300
STRADIPNE	FKKNVGFKKVLAFEFANNRKFMHLDTVFTMVDYDKFTIHPEIEGDLHVYS	300
STRADIPYR	YSVTYDNEELHIVEEKGD LAELLAANLGVEKVDLIRCGGDNLVAAGREQW	350
STRADIPNE	VTYENEKLIKIVEEKGD LAELLAQNLGVEKVHLIRCGGNIVAAAREQWND	350
STRADIPYR	NDGSNTLTIAPGVVVVYNRNTITNAILESKGLKLIKIHGSELVRGRGGPR	400
STRADIPNE	GSNTLTIAPGVVVVYDRNTVTNKILEEYGLRLIKIRGSELVRGRGGPRCM	400
STRADIPYR	CMSMPFEREDI	411
STRADIPNE	SMPFEREEV	409

FIG. 10

STRADIPYR = *Streptococcus pyogenes*

STRADIPNE = *Streptococcus pneumoniae*

The alignment was done on 2 amino acid sequences. 8/10

Alignment

BORADIBUR	MEEEYLNPNIFSEIGRLKKVLLHRPGELENLTPLIMKNFLFDDIPYLK	50
BORADIAFZ	MEEYLNPNIFSEIGRLKKVLLHRPGELENLTPFIMKNFLFDDIPYLEV	50
BORADIBUR	VARQEHEVFVNILKDNSVEIEYVEDLVSEVLASSVALKNKFISQFILEAE	100
BORADIAFZ	ARQEHEVFASILKNNLVEIEYIEDLISEVLVSSVALENKFISQFILEAEI	100
BORADIBUR	IKTDGVINILKDYFSNLTVDNMVSKMISGVAREELKDCEFSLDDWVNGSS	150
BORADIAFZ	KTDFTINLLKDYFSSLTIDNMISKMISGVVTEELKNYTSSLDDLNGANL	150
BORADIBUR	FVIDPMPNVLFTRDPFASIGNGITINKMYTKVRRRETIFAHEYIFKYHSAY	200
BORADIAFZ	FIIDPMPNVLFTRDPFASIGNGVTTNKMFVKVRQRETIFAHEYIFKYHPVY	200
BORADIBUR	KENVPIWFNRWEETSLEGGDEFVLNKDLLVIGISERTEAGSVEKLAASLF	250
BORADIAFZ	KENVPIWLNRWEEASLEGGDELVLNKGLLVIGISERTEAKSVEKLAISLF	250
BORADIBUR	KNKAPFSTILAFKIPKNRAYMHLDTVFTQIDYSVFTSFTSDDMYFSIYVL	300
BORADIAFZ	KNKTSFDITLAFQIPKNRSYMHLDTVFTQIDYSVFTSFTSDDMYFSIYVL	300
BORADIBUR	TYNSNSNKNIKKEKAKLKDVLFSYLGRKIDIICAGGDLIHGAREQWND	350
BORADIAFZ	TYNPSSSKIHIKKEKARIKDVLFSYLGRKIDIICAGGDLIHGAREQWND	350
BORADIBUR	GANVLAIAPGEVIAYSRNHVTNKLFEENGIVHRIPSSSELSRGRGGPRCM	400
BORADIAFZ	GANVLAIAPGEIAYSRNHVTNKLFEENGIVHRIPSSSELSRGRGGPRCM	400
BORADIBUR	SMSLVREDI	409
BORADIAFZ	SMPLIREDI	409

FIG. 11

BORADIBUR = *Borrelia burgdorferi*
 BORADIAFZ = *Borrelia afzelii*

The alignment was done on 3 amino acid sequences.

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Alignment

QIAADIINT	MTDFSKDKEKLAQATQGGENERAEIVVVHLPQGTSLTSLNPEGNNLEEP	50
CLOADIPER	MRDDRALNVTSEIGRLKTVLLHRPGEEIENLTPDLLDRLLFDDIPYLKVA	50
BACADILIC	MIMTTPIHVYSEIGPLKTVMLKRPGRELENLTPEYLERLLFDDIPFLPAV	50
QIAADIINT	ICPDELRRDHEGFQAVLKEKGCRVYMPYDVLSEASPAEREVLMDQAMASL	100
CLOADIPER	REEHDAFAQTLREAGVEVLYLEVLAEEAIETSDEVKQQFISEFIDEAGVE	100
BACADILIC	QKEHDQFAETLKQQGAEVLYLEKLTAEALDDALVREQFIDELLTESKADI	100
QIAADIINT	KYELHATGARITPKMKYCVSDEYKRKVL SALSTRNLVDVILSEPVHILAP	150
CLOADIPER	SERLKEALIEYFNSFSDNKAMVDKMMAGVRKEELKDYHRESLYDQVNNVY	150
BACADILIC	NGAYDRLKEFLLTFDADSMVEQVMGIRKNELEREKKSHLHELMEDHYPF	150
QIAADIINT	GVRNTALVTNSVEIHDSNNMVFMRDQQITTRRGIVMGQFQAPORRREQVL	200
CLOADIPER	PFVCDPMPNLYFTREPFA TIGHGITLNMRTDTRNRETIFAKYIFRHHPR	200
BACADILIC	YLDPMPNLYFTRDPA AIGSGLTINKMKEPARRRESLFMRYIINHHPRFK	200
QIAADIINT	ALIFWKRLGARVVGDCREGGPHCMLEGGDFVPVSPGLAMMGVGLRSTYVG	250
CLOADIPER	FEGKDIPFWFNRNDKTSLEGGDELILSKEILAVGISQRTDSASVEKLAKK	250
BACADILIC	GHEIPVWLDRDFKFNIEGGDELVLNEETVAIGVSERTTAQAIERLVRNLF	250
QIAADIINT	AQYLMSKDLLGTRRFVVKDCFDQHQDRMHL DCTFVLHDKLVVLD DDIYIC	300
CLOADIPER	LLYYPDTSFKTVLAFKIPVSRAFMHLDTVFTQVDYDKFTVHPGIVGPLEV	300
BACADILIC	QRQSRIRRVLA VEIPKSRAFMHLDTVFTMVDRDQFTIHPAIQGPEGDMRI	300
QIAADIINT	SGMGLRYVDEWIDVGADAVKKAKSSAVTCGNYVLAKANVEFQQWLSSENGY	350
CLOADIPER	YALTKDPENDGQLLVTEEVD TLENILKKYLD RDIKLIKCGGGDEIIAARE	350
BACADILIC	FVLERGKTADEIHTTEEHN LPEVLKRTLGLSDVNLIFCGGGDEIASAREQ	350
QIAADIINT	TIVRIPHEYQLAYGCNNLNLGNNCVLSVHQPTVDFIKADPAYISYCKSNN	400
CLOADIPER	QWNDGSNTLAIAPGEVVVYSRNYVTNEILEKEGIKLHVIPSSSELSRGRGG	400
BACADILIC	WNDGSNTLAIAPGVVVYDRNYISNECLREQGIKVIEIPSGELSRGRGGP	400
QIAADIINT	LPNGLDLVYVPFRGITRMYGSLHCASQVVYRTPLAPAAVKACEQEGDGIA	450
CLOADIPER	PRCMSMPLIREDL	413
BACADILIC	RCMSMPLYREDVK	413
QIAADIINT	AIYEKNGEPVDAAGKKFDCVIYIPSSVDDLIDGLKINLRDDAAPSREIIA	500
QIAADIINT	DAYGLYQKLVSEGRVPYITWRMPSPMPVVS LKGAAGAGSLKAVLDKIPQLT	550
QIAADIINT	PFTPKAVEGAPAA YTRYLGLEQADICVDIK	580

QIAADIINT = *Qiardia intestinalis*
 CLOADIPER = *Clostridium perfringens*
 BACADILIC = *Bacillus licheniformis*

FIG. 12

The alignment was done on 2 amino acid sequences.

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Alignment

ENTADIFAE	MSHPINVFSEIGKLKTVMLHRPGKELENLMPDYLERLLFDDIPFLEKAQA	50
LACADISAK	MTSPIHVNSEIGKLKTVLLKRPGEVENITPDIMYRLLFDDIPYLPTIQK	50
ENTADIFAE	EHDFAEALLRSKDIEVVYLEDLAAEALINEEVRRQFIDQFLEENIRSES	100
LACADISAK	EHDQFAQTLRDNGVEVLYLENLAAEAIDAGDVKEAFLDKMLNESHKSPQ	100
ENTADIFAE	AKEKVRELMLEIDDNEELIQKAIAGIQKQELPKYEQEFLTDMVEADYPFI	150
LACADISAK	VQAALKDYLISMATLDMVEKIMAGVRTNEIDIKSKALIDVSADDDYPFYM	150
ENTADIFAE	IDPMPNLYFTRDNFATMGHGISLNHMYSVTRQRETIFGQYIFDYHPRFAG	200
LACADISAK	DPMPNLYFTRDPAASMGDGLTINKMTFEARQRESMFMEVIMQHHPRFANQ	200
ENTADIFAE	KEVPRVYDRSESTRIEGGDELILSKEVVAIGISORTDAASIEKIARNIFE	250
LACADISAK	GAQVWRDRDHIDRMEGGDELILSDKVLAIGISQRTSAQSIEELAKVLFAN	250
ENTADIFAE	QKLGFKNILAFDIGEHRKFMHLDTVFTMIDYDKFTIHPEIEGGLVVYSIT	300
LACADISAK	HSGFEKILAIKIPHKHAMMHLDTVFTMIDYDKFTIHPIQGAGGMVDTYI	300
ENTADIFAE	EKADGDIQITKEKDTLDNILCKYLHLDNVQLIRCGAGNLTAAAREQWNDG	350
LACADISAK	LEPGNNDKIKITHQTDLEKVLRLDALEVPELTLIPCGGGDAVVAPREQWND	350
ENTADIFAE	SNTLAIAPGEVVVYDRNTITNKALEEAGVKLNYPGSELVRGRGGPRCMS	400
LACADISAK	GSNTLAIAPGVVVYDRNYVSNNLRQYGIKVIEVPSSSELSRGRGGPRCM	400
ENTADIFAE	MPLYREDL	408
LACADISAK	SMPLVRRKT	409

FIG. 13

ENTADIFAE = *Enterococcus faecalis*

LACADISAK = *Lactobacillus sake*